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List of Publications by Year
in descending order

Version: 2024-02-01

23 papers	863 citations	623734 14 h-index	642732 23 g-index
23 all docs	23 docs citations	23 times ranked	2469 citing authors

#	Article	IF	Citations
1	Dynamic long-range chromatin interactions controlMybproto-oncogene transcription during erythroid development. EMBO Journal, 2012, 31, 986-999.	7.8	119
2	Whole-transcriptome analysis of endothelial to hematopoietic stem cell transition reveals a requirement for Gpr56 in HSC generation. Journal of Experimental Medicine, 2015, 212, 93-106.	8.5	105
3	Engram-specific transcriptome profiling of contextual memory consolidation. Nature Communications, 2019, 10, 2232.	12.8	83
4	Whole exome sequencing coupled with unbiased functional analysis reveals new Hirschsprung disease genes. Genome Biology, 2017, 18, 48.	8.8	72
5	Exome sequencing and functional analyses suggest that SIX6 is a gene involved in an altered proliferationâ€“differentiation balance early in life and optic nerve degeneration at old age. Human Molecular Genetics, 2014, 23, 1320-1332.	2.9	63
6	Paroxysmal exercise-induced dystonia within the phenotypic spectrum ofECHS1deficiency. Movement Disorders, 2016, 31, 1041-1048.	3.9	58
7	Next-generation sequencing-based genome diagnostics across clinical genetics centers: implementation choices and their effects. European Journal of Human Genetics, 2015, 23, 1142-1150.	2.8	56
8	PLD3 variants in population studies. Nature, 2015, 520, E2-E3.	27.8	49
9	Next generation sequencing of SNPs for non-invasive prenatal diagnosis: challenges and feasibility as illustrated by an application to Î²-thalassaemia. European Journal of Human Genetics, 2013, 21, 1403-1410.	2.8	47
10	CTCF chromatin residence time controls three-dimensional genome organization, gene expression and DNA methylation in pluripotent cells. Nature Cell Biology, 2021, 23, 881-893.	10.3	30
11	Genetic variants in RBFOX3 are associated with sleep latency. European Journal of Human Genetics, 2016, 24, 1488-1495.	2.8	27
12	Nonsynonymous Variation in NKPD1 Increases Depressive Symptoms in European Populations. Biological Psychiatry, 2017, 81, 702-707.	1.3	26
13	Deciphering the RNA landscape by RNAome sequencing. RNA Biology, 2015, 12, 30-42.	3.1	23
14	A functional variant in the miRâ€142 promoter modulating its expression and conferring risk of Alzheimer disease. Human Mutation, 2019, 40, 2131-2145.	2.5	23
15	Characterization of the ferret TRB locus guided by V, D, J, and C gene expression analysis. Immunogenetics, 2020, 72, 101-108.	2.4	14
16	Regulation of the cohesin-loading factor NIPBL: Role of the lncRNA NIPBL-AS1 and identification of a distal enhancer element. PLoS Genetics, 2017, 13, e1007137.	3.5	14
17	Unbiased Interrogation of 3D Genome Topology Using Chromosome Conformation Capture Coupled to High-Throughput Sequencing (4C-Seq). Methods in Molecular Biology, 2017, 1507, 199-220.	0.9	11
18	Targeted chromatin conformation analysis identifies novel distal neural enhancers of ZEB2 in pluripotent stem cell differentiation. Human Molecular Genetics, 2020, 29, 2535-2550.	2.9	10

#	Article	IF	Citations
19	Global quantitative proteomics reveals novel factors in the ecdysone signaling pathway inDrosophila melanogaster. Proteomics, 2015, 15, 725-738.	2.2	9
20	Exome-Wide Meta-Analysis Identifies Rare 3â€²-UTR Variant in ERCC1/CD3EAP Associated with Symptoms of Sleep Apnea. Frontiers in Genetics, 2017, 8, 151.	2.3	7
21	Molecular analysis of the erythroid phenotype of a patient with BCL11A haploinsufficiency. Blood Advances, 2021, 5, 2339-2349.	5.2	7
22	The dystrophin gene and cognitive function in the general population. European Journal of Human Genetics, 2015, 23, 837-843.	2.8	6
23	Exome Sequencing Analysis Identifies Rare Variants in ATM and RPL8 That Are Associated With Shorter Telomere Length. Frontiers in Genetics, 2020, 11, 337.	2.3	4